

SEQUENCE LISTING



SEP 20 2001

JC63

<110> Scott, Fred

<120> Recombinant Multivalent Viral Vaccine

<130> 18617.0016

<140> US 09/873,881

<141> 2001-06-04

<150> US 08/552,369

<151> 1995-11-03

<160> 19

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<212> DNA

<213> feline panleukopenia virus

<220>

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aga aat gaa aga gct aca gga tct ggg aac ggg tct gga ggc ggg 90  
Arg Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly  
20 25 30

ggt ggt ggt tct ggg ggt gtg ggg att tct acg ggt act ttc 135  
Gly Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe  
35 40 45

aat aat cag acg gaa ttt aaa ttt ttg gaa aac gga tgg gtg gaa 180  
Asn Asn Gln Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu  
50 55 60

atc aca gca aac tca agc aga ctt gta cat tta aat atg cca gaa 225  
Ile Thr Ala Asn Ser Ser Arg Leu Val His Leu Asn Met Pro Glu  
65 70 75

agt gaa aat tat aaa aga gta gtt gta aat aat atg gat aaa act 270  
Ser Glu Asn Tyr Lys Arg Val Val Val Asn Asn Met Asp Lys Thr  
80 85 90

gca gtt aaa gga aac atg gct tta gat gac act cat gta caa att 315  
Ala Val Lys Gly Asn Met Ala Leu Asp Asp Thr His Val Gln Ile  
95 100 105

gta aca cct tgg tca ttg gtt gat gca aat gct tgg gga gtt tgg 360  
Val Thr Pro Trp Ser Leu Val Asp Ala Asn Ala Trp Gly Val Trp  
110 115 120

ttt aat cca gga gat tgg caa cta att gtt aat act atg agt gag	405
Phe Asn Pro Gly Asp Trp Gln Leu Ile Val Asn Thr Met Ser Glu	
125 130 135	
ttg cat tta gtt agt ttt gaa caa gaa att ttt aat gtt gtt tta	450
Leu His Leu Val Ser Phe Glu Gln Glu Ile Phe Asn Val Val Leu	
140 145 150	
aag act gtt tca gaa tct gct act cag cca cca act aaa gtt tat	495
Lys Thr Val Ser Glu Ser Ala Thr Gln Pro Pro Thr Lys Val Tyr	
155 160 165	
aat aat gat tta act gca tca ttg atg gtt gca tta gat agt aat	540
Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala Leu Asp Ser Asn	
170 175 180	
aat act atg cca ttt act cca gca gct atg aga tct gag aca ttg	585
Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser Glu Thr Leu	
185 190 195	
ggg ttt tat cca tgg aaa cca acc ata cca act cca tgg aga tat	630
Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp Arg Tyr	
200 205 210	
tat ttt caa tgg gat aga aca tta ata cca tct cat act gga act	675
Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly Thr	
215 220 225	
agt ggc aca cca aca aat ata tat cat ggt aca gat cca gat gat	720
Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp	
230 235 240	
gtt caa ttt tat act att gaa aat tct gtg cca gta cac tta cta	765
Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu	
245 250 255	
aga aca ggt gat gaa ttt gct aca gga aca ttt ttt ttt gat tgt	810
Arg Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys	
260 265 270	
aaa cca tgt aga cta aca cat aca tgg caa aca aac aga gca ttg	855
Lys Pro Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu	
275 280 285	
ggc tta cca cca ttt cta aat tct ttg cct caa tct gaa gga gct	900
Gly Leu Pro Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala	
290 295 300	
act aac ttt ggt gat ata gga gtt caa caa gat aaa aga cgt ggt	945
Thr Asn Phe Gly Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly	
305 310 315	
gta act caa atg gga aat aca gac tat att act gaa gct act att	990
Val Thr Gln Met Gly Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile	

320	325	330	
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cgg ggg gga gcg caa aca gat gaa aat caa gca gca gat ggt gat Arg Gly Gly Ala Gln Thr Asp Glu Asn Gln Ala Ala Asp Gly Asp 365	370	375	1125
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aca gga gaa aca cct gag aga ttt aca tat ata gca cat caa gat Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr Ile Ala His Gln Asp 395	400	405	1215
aca gga aga tat cca gca gga gat tgg att caa aat att aac ttt Thr Gly Arg Tyr Pro Ala Gly Asp Trp Ile Gln Asn Ile Asn Phe 410	415	420	1260
aac ctt cct gta aca aat gat aat gta ttg cta cca aca gat cca Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro Thr Asp Pro 425	430	435	1305
att gga ggt aaa aca gga atc aac tat act aat ata ttt aat act Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe Asn Thr 440	445	450	1350
tat ggt cct tta act gca tta aat aat gta cca cca gtt tat cca Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr Pro 455	460	465	1395
aat ggt caa att tgg gat aaa gaa ttt gat act gac tta aaa cca Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro 470	475	480	1440
aga ctt cat gta aat gca cca ttt gtt tgt caa aat aat tgt cct Arg Leu His Val Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro 485	490	495	1485
ggt caa tta ttt gta aaa gtt gcg cct aat tta aca aat gaa tat Gly Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr 500	505	510	1530
gat cct gat gca tct gct aat atg tca aga att gta act tac tca Asp Pro Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser 515	520	525	1575
gat ttt tgg tgg aaa ggt aaa tta gta ttt aaa gct aaa cta aga			1620

Asp Phe Trp Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg	530	535	540	
gca tct cat act tgg aat cca att caa caa atg agt att aat gta Ala Ser His Thr Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val	545	550	555	1665
gat aac caa ttt aac tat cta cca aat aat att gga gct atg aaa Asp Asn Gln Phe Asn Tyr Leu Pro Asn Asn Ile Gly Ala Met Lys	560	565	570	1710
att gta tat gaa aaa tct caa cta gca cct aga aaa tta tat Ile Val Tyr Glu Lys Ser Gln Leu Ala Pro Arg Lys Leu Tyr	575	580		1752
taatatactt actatgtttt tatggttatt acatatcaac tagcacctag				1802
aaaattatat taatatactt actatgtttt tatgtttatt acatattatt				1852
ttaagattaa ttaaattaca acatagaaat attgtacttg tatttgatat				1902
aggatttaga aggtttgtta tatggtatac aataactgta agaaatagaa				1952
gaacatttag atcatggtta gtatggata caataactgt aagaaataga				2002
agaacattta gatcatggtt agtagttgt tttataaaat gtaattgtaa				2052
actattaatg tatgttgtta tggtgtgggt ggttgggtgg tttgccctta				2102
gaatatgtta aggaccaaaa aaatcaataa aagacattta aaacttaatg				2152
gtctcgata ctgtctataa ggtgaactaa cttaccata agtataact				2202
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tg				2254

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cca ttg tgt ttt ggg aaa ttc cct att tac acg ata cta gac				84
Pro Leu Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Leu Asp				
15	20	25		

aag ctt ggt ccc tgg agc ccg att gac ata cat cac ctc agc	126
Lys Leu Gly Pro Trp Ser Pro Ile Asp Ile His His Leu Ser	
30 35 40	
tgc cca aac aat ttg gta gtg gag gac gaa gga tgc acc aac	168
Cys Pro Asn Asn Leu Val Val Glu Asp Glu Gly Cys Thr Asn	
45 50 55	
ctg tca ggg ttc tcc tac atg gaa ctt aaa gtt gga tac atc	210
Leu Ser Gly Phe Ser Tyr Met Glu Leu Lys Val Gly Tyr Ile	
60 65 70	
tta gcc ata aaa atg aac ggg ttc act tgc aca ggc gtt gtg	252
Leu Ala Ile Lys Met Asn Gly Phe Thr Cys Thr Gly Val Val	
75 80	
acg gag gct gaa acc tac act aac ttc gtt ggt tat gtc aca	294
Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr Val Thr	
85 90 95	
acc acg ttc aaa aga aag cat ttc cgc cca aca cca gat gca	336
Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala	
100 105 110	
tgt aga gcc gcg tac aac tgg aag atg gcc ggt gac ccc aga	378
Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg	
115 120 125	
tat gaa gag tct cta cac aat ccg tac cct gac tac cgc tgg	420
Tyr Glu Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr Arg Trp	
130 135 140	
ctt cga act gta aaa acc acc aag gag tct ctc gtt atc ata	462
Leu Arg Thr Val Lys Thr Lys Glu Ser Leu Val Ile Ile	
145 150	
tct cca agt gta gca gat ttg gac cca tat gac aga tcc ctt	504
Ser Pro Ser Val Ala Asp Leu Asp Pro Tyr Asp Arg Ser Leu	
155 160 165	
cac tcg agg gtc ttc cct agc ggg aag tgc tca gga gta gcg	546
His Ser Arg Val Phe Pro Ser Gly Lys Cys Ser Gly Val Ala	
170 175 180	
gtg tct tct acc tac tgc tcc act aac cac gat tac acc att	588
Val Ser Ser Thr Tyr Cys Ser Thr Asn His Asp Tyr Thr Ile	
185 190 195	
tgg atg ccc gag aat ccg aga cta ggg atg tct tgt gac att	630
Trp Met Pro Glu Asn Pro Arg Leu Gly Met Ser Cys Asp Ile	
200 205 210	
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Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Lys Gly Ser Glu	

215	220	
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aaa gga gca tgc aaa ctc aag tta tgt gga gtt cta gga ctt		756
Lys Gly Ala Cys Lys Leu Lys Leu Cys Gly Val Leu Gly Leu		
240	245	250
aga ctt atg gat gga aca tgg gtc gcg atg caa aca tca aat		798
Arg Leu Met Asp Gly Thr Trp Val Ala Met Gln Thr Ser Asn		
255	260	265
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Glu Thr Lys Trp Cys Pro Pro Asp Gln Leu Val Asn Leu His		
270	275	280
gac ttt cgc tca gac gaa att gag cac ctt gtt gta gag gag		882
Asp Phe Arg Ser Asp Glu Ile Glu His Leu Val Val Glu Glu		
285	290	
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Leu Val Arg Lys Arg Glu Glu Cys Leu Asp Ala Leu Glu Ser		
295	300	305
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Ile Met Thr Thr Lys Ser Val Ser Phe Arg Arg Leu Ser His		
310	315	320
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Leu Arg Lys Leu Val Pro Gly Phe Gly Lys Ala Tyr Thr Ile		
325	330	335
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Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser		
340	345	350
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Val Arg Thr Trp Asn Glu Ile Leu Pro Ser Lys Gly Cys Leu		
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Arg Val Gly Gly Arg Cys His Pro His Val Asn Gly Val Phe		
365	370	375
ttc aat ggt ata ata tta gga cct gac ggc aat gtc tta atc		1176
Phe Asn Gly Ile Ile Leu Gly Pro Asp Gly Asn Val Leu Ile		
380	385	390
cca gag atg caa tca tcc ctc ctc cag caa cat atg gag ttg		1218
Pro Glu Met Gln Ser Ser Leu Leu Gln Gln His Met Glu Leu		
395	400	405
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Leu	Glu	Ser	Ser	Val	Ile	Pro	Leu	Val	His	Pro	Leu	Ala	Asp	
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Pro	Ser	Thr	Val	Phe	Lys	Asp	Gly	Asp	Glu	Ala	Glu	Asp	Phe	
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Val	Glu	Val	His	Leu	Pro	Asp	Val	His	Asn	Gln	Val	Ser	Gly	
435					440					445				
gtt	gac	ttg	ggt	ctc	ccg	aac	tgg	ggg	aag	tat	gta	tta	ctg	1386
Val	Asp	Leu	Gly	Leu	Pro	Asn	Trp	Gly	Lys	Tyr	Val	Leu	Leu	
450					455					460				
agt	gca	ggg	gcc	ctg	act	gcc	ttg	atg	ttg	ata	att	ttc	ctg	1428
Ser	Ala	Gly	Ala	Leu	Thr	Ala	Leu	Met	Leu	Ile	Ile	Phe	Leu	
465					470						475			
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Met	Thr	Cys	Cys	Arg	Arg	Val	Asn	Arg	Ser	Glu	Pro	Thr	Gln	
480					485						490			
cac	aat	ctc	aga	ggg	aca	ggg	agg	gag	gtg	tca	gtc	act	ccc	1512
His	Asn	Leu	Arg	Gly	Thr	Gly	Arg	Glu	Val	Ser	Val	Thr	Pro	
495					500									
caa	agc	ggg	aag	atc	ata	tct	tca	tgg	gaa	tca	cac	aag	agt	1554
Gln	Ser	Gly	Lys	Ile	Ile	Ser	Ser	Trp	Glu	Ser	His	Lys	Ser	
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Gly	Gly	Glu	Thr	Arg	Leu									
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<212> DNA
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<220>
<223> sequencing primer

<400> 6
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Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val
20 25 30

ggc ttc tgc gat aac cct tta atg tgt tgt tat cct gaa tta cta 135
Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu
35 40 45

cct gaa ttt ggc acc atg tgg gat tgt gat caa tcg cca ctc caa 180
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gcc gga aaa atc ttc caa cca cac cct ggc gtc ctt atg cat cac Ala Gly Lys Ile Phe Gln Pro His Pro Gly Val Leu Met His His 95 100 105			315
ctc atc tgt aag gtt gca gaa gga tgg gac cca aac ctg cca ctt Leu Ile Cys Lys Val Ala Glu Gly Trp Asp Pro Asn Leu Pro Leu 110 115 120			360
ttc cgc ttg gaa gcg gac gat ggt tcc atc acg aca cct gaa cag Phe Arg Leu Glu Ala Asp Asp Gly Ser Ile Thr Thr Pro Glu Gln 125 130 135			405
gga aca atg gtt ggt gga gtc att gct gag ccc aac gcc caa atg Gly Thr Met Val Gly Gly Val Ile Ala Glu Pro Asn Ala Gln Met 140 145 150			450
tca acc gca gct gac atg gcc act ggg aaa agt gtg gac tct gag Ser Thr Ala Ala Asp Met Ala Thr Gly Lys Ser Val Asp Ser Glu 155 160 165			495
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gat cct gtt caa agt act tca atg ctg caa tat cct cat gtc ctc Asp Pro Val Gln Ser Thr Ser Met Leu Gln Tyr Pro His Val Leu 245 250 255			765
ttt gat gct cgt caa gtt gaa cct gtt atc ttt tcc att ccc gat			810

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Asn	Asp	Ser	Asn	Ser	Ser	Gly	Cys	Ile	Val	Thr	Val	Glu	Thr	Lys	
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ccg	ggg	cca	gat	ttc	aag	ttt	cac	ctc	tta	aaa	cct	cct	ggg	tct	990
Pro	Gly	Pro	Asp	Phe	Lys	Phe	His	Leu	Leu	Lys	Pro	Pro	Gly	Ser	
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Phe	Val	Ile	Arg	Pro	Phe	Val	Phe	Gln	Ala	Asn	Arg	His	Phe	Asp	
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ccc	gac	aca	aca	atc	cca	ggt	gag	ttg	gta	cct	gtt	ggt	gac	tat	1305
Pro	Asp	Thr	Thr	Ile	Pro	Gly	Glu	Leu	Val	Pro	Val	Gly	Asp	Tyr	
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gcc	atc	act	aat	ggc	acc	aac	aat	gat	atc	acc	aca	gct	gcg	cag	1350
Ala	Ile	Thr	Asn	Gly	Thr	Asn	Asn	Asp	Ile	Thr	Thr	Ala	Ala	Gln	
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tac	gat	gca	gcc	act	gag	att	aga	aac	aac	acc	aat	ttc	aga	ggc	1395
Tyr	Asp	Ala	Ala	Thr	Glu	Ile	Arg	Asn	Asn	Thr	Asn	Phe	Arg	Gly	
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470 475 480	
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Ile Ser Asn Thr Ala Phe Ile Thr Thr Gly Thr Val Asp Gly Ala	
485 490 495	
aaa ttg ata ccc agt aat acc att gac caa aca aaa att gcc gta	1530
Lys Leu Ile Pro Ser Asn Thr Ile Asp Gln Thr Lys Ile Ala Val	
500 505 510	
ttc caa gac aca cat gcg aat aag cat gtc cag acc tcg gac gac	1575
Phe Gln Asp Thr His Ala Asn Lys His Val Gln Thr Ser Asp Asp	
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Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu Glu Ala Ile	
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Gly Ala Asp Arg Asp Arg Val Val Arg Ile Ser Val Leu Pro Glu	
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cgt ggc gca cgt ggt ggc aat cac cca atc ttc cac aaa aac tct	1710
Arg Gly Ala Arg Gly Gly Asn His Pro Ile Phe His Lys Asn Ser	
560 565 570	
atc aag ctt ggt tat gta att agg tcc att gat gtg ttc aat tct	1755
Ile Lys Leu Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser	
575 580 585	
caa att ctg cat acc tct agg caa ctt tcc ctc aat cat tac tta	1800
Gln Ile Leu His Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu	
590 595 600	
ttg tcg cct gac tcc ttt gct gtc tat agg att att gac tct aat	1845
Leu Ser Pro Asp Ser Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn	
605 610 615	
gga tcc tgg ttt gac ata ggc att gat aat gat gga ttt tct ttt	1890
Gly Ser Trp Phe Asp Ile Gly Ile Asp Asn Asp Gly Phe Ser Phe	
620 625 630	
gtt ggt gta tca agt att ggt aaa tta gag ttt cct tta act gcc	1935
Val Gly Val Ser Ser Ile Gly Lys Leu Glu Phe Pro Leu Thr Ala	
635 640 645	
tcc tac atg gga att caa ttg gca aaa att cga ctt gcc tct aac	1980
Ser Tyr Met Gly Ile Gln Leu Ala Lys Ile Arg Leu Ala Ser Asn	
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att agg agt gtg atg aca aaa tta tga	2007
Ile Arg Ser Val Met Thr Lys Leu	
665	

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<211> 582
<212> DNA
<213> artificial sequence

<220>
<223> hemagglutinin left arm

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atattgtac tatcgatagt atatacaacc aaacctcatc ctacacagat      200
atcaaaaaaa ctaggcgatg atgctactct atcgtgtaat agaaaacaata      250
cacatggata tcttgtcatg agttcttggt ataagaaacc agactccatt      300
attctcttag cagccaaaaa cgatgtcgta tactttgatg attatacagc      350
ggataaaagta tcatacgatt caccgtatga tactctagct acaattatta      400
caattaaatc attgacatct gcagatgcag gtacttataat atgcgcattc      450
tttataacat caacaaatga tacggataaa atagattatg aagaatactt      500
catagatttgc gttgtaaatc cagctaattgt atccactatt gacgcgattc      550
tatcaggatc taatttctcc gtgataggta tc                           582

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<211> 447
<212> DNA
<213> artificial sequence

<220>
<223> hemagglutinin right arm

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acaatatcta ctacaaaata tacaactagt gactttatag agatattttgg      150
cattgttca ctaattttat tattggccgt ggcgatttc tgtatttat      200
tatttctgttca gtggacggtc tcgtaaacaa gaaacaaaata tattatagat      250
tttaactcag ataaaatgtct ggaataatta aatctatcgt tttgagcggta      300
ccatctgggtt ccggcaagac agctatacgta aggagactct tacaagattt      350
tggaaatata tttggatttgc tggtatccca taccactaga ttccctcgcc      400
ctatggaaacg agaaggtgtc gactaccatt acgttaacag agaggcc      447

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<211> 40
<212> DNA
<213> artificial sequence

<220>
<223> primer P3

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<220>
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<400> 11
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<220>
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<220>
<223>

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atg aag tac att ttg cta ata ctc gcg tgc ata att gca tgc gtt 96
Met Lys Tyr Ile Leu Ile Leu Ala Cys Ile Ile Ala Cys Val
1 5 10 15

tat ggt gaa cgc tac tgt gcc atg caa gac agt ggc ttg cag tgt 141
Tyr Gly Glu Arg Tyr Cys Ala Met Gln Asp Ser Gly Leu Gln Cys
20 25 30

att aat ggc aca aat tca aga tgt caa acc tgc ttt gaa cgt ggt 186
Ile Gln Gly Thr Gln Ser Arg Cys Gln Thr Cys Phe Glu Arg Gly
35 40 45

gat ctt att tgg cat ctt gct aac tgg aac ttc agc tgg tct gta 231
Asp Leu Ile Trp His Leu Ala Asn Trp Asn Phe Ser Trp Ser Val
50 55 60

ata ttg att gtt ttt ata aca gtg tta caa tat ggc aga cca caa 276
Ile Leu Ile Val Phe Ile Thr Val Leu Gln Tyr Gly Arg Pro Gln
65 70 75

ttt agc tgg ctc gtt tat ggc att aaa atg ctg atc atg tgg cta 321
Phe Ser Trp Leu Val Tyr Gly Ile Lys Met Leu Ile Met Trp Leu
80 85 90

tta tgg cct att gtt cta gcg ctt acg att ttt aat gca tac tct 366
Leu Trp Pro Ile Val Leu Ala Leu Thr Ile Phe Asn Ala Tyr Ser
95 100 105

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Glu Tyr Gln Val Ser Arg Tyr Val Met Phe Gly Phe Ser Val Ala	
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Gly Ala Val Val Thr Phe Ala Leu Trp Met Met Tyr Phe Val Arg	
125 130 135	
tct gtt cag cta tat aga aga acc aaa tca tgg tgg tct ttt aat	501
Ser Val Gln Leu Tyr Arg Arg Thr Lys Ser Trp Trp Ser Phe Asn	
140 145 150	
cct gag act aat gca att ctt tgt gtt aat gca ttg ggt aga agt	546
Pro Glu Thr Asn Ala Ile Leu Cys Val Asn Ala Leu Gly Arg Ser	
155 160 165	
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Tyr Val Leu Pro Leu Asp Gly Thr Pro Thr Gly Val Thr Leu Thr	
170 175 180	
cta ctt tca gga aat cta tat gct gaa ggt ttc aaa atg gct ggt	636
Leu Leu Ser Gly Asn Leu Tyr Ala Glu Gly Phe Lys Met Ala Gly	
185 190 195	
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Gly Leu Thr Ile Glu His Leu Pro Lys Tyr Val Met Ile Ala Thr	
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Pro Ser Arg Thr Ile Val Tyr Thr Ile Val Gly Lys Gln Leu Lys	
215 220 225	
gca act act gcc aca gga tgg gct tac tac gta aaa tct aaa gct	771
Ala Thr Thr Ala Thr Gly Trp Ala Tyr Tyr Val Lys Ser Lys Ala	
230 235 240	
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Lys	Arg	Arg	Gly	Arg	Ser	Asn	Ser	Arg	Gly	Arg	Lys	Asn	Asn	Asn	Asp	
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Ile	Pro	Leu	Ser	Phe	Tyr	Asn	Phe	Ile	Thr	Leu	Glu	Gln	Glu	Ser		
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Gly	Asn	Lys	Asp	Gln	Gln	Ile	Gly	Tyr	Trp	Asn	Arg	Gln	Ile	Arg		
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Tyr	Arg	Ile	Val	Lys	Gly	Gln	Arg	Lys	Glu	Leu	Ala	Glu	Arg	Trp		
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ttc	ttt	tac	ttc	tta	ggt	aca	gga	cct	cat	gct	gat	gct	aaa	ttc		315
Phe	Phe	Tyr	Phe	Leu	Gly	Thr	Gly	Phe	His	Ala	Asp	Ala	Lys	Phe		
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Lys	Asp	Lys	Ile	Asp	Gly	Val	Phe	Trp	Val	Ala	Arg	Asp	Gly	Ala		
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Met	Asn	Lys	Pro	Thr	Thr	Leu	Gly	Thr	Arg	Gly	Thr	Asn	Asn	Glu		
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Ser	Lys	Pro	Leu	Arg	Phe	Asp	Gly	Lys	Ile	Pro	Pro	Gln	Phe	Gln		
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Leu	Glu	Val	Asn	Arg	Ser	Arg	Asn	Asn	Ser	Arg	Ser	Gly	Ser	Gln		
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tct	aga	tct	gtt	tca	aga	aac	aga	tct	caa	tct	aga	gga	aga	cac		540
Ser	Arg	Ser	Val	Ser	Arg	Asn	Arg	Ser	Gln	Ser	Arg	Gly	Arg	His		
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cat	tcc	aat	aac	cag	aat	aat	aat	gtt	gag	gat	aca	att	gta	gcc		585
His	Ser	Asn	Asn	Gln	Asn	Asn	Asn	Val	Glu	Asp	Thr	Ile	Val	Ala		
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gtg	ctt	gaa	aaa	tta	ggt	gtt	act	gac	aaa	caa	agg	tca	cgt	tct		630
Val	Leu	Glu	Lys	Leu	Gly	Val	Thr	Asp	Lys	Gln	Arg	Ser	Arg	Ser		
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Lys Pro Arg Glu Arg Ser Asp Ser Lys Pro Arg Asp Thr Thr Pro	
215 220 225	
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Lys Asn Ala Asn Lys His Thr Trp Lys Lys Thr Ala Gly Lys Gly	
230 235 240	
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Asp Val Thr Thr Phe Tyr Gly Ala Arg Ser Ser Ser Ala Asn Phe	
245 250 255	
ggt gat agt gat ctc gtt gcc aat ggt aac gct gcc aaa tgc tac	810
Gly Asp Ser Asp Leu Val Ala Asn Gly Asn Ala Ala Lys Cys Tyr	
260 265 270	
cct cag ata gct gaa tgt gtt cca tca gtg tct agc ata atc ttt	855
Pro Gln Ile Ala Glu Cys Val Pro Ser Val Ser Ser Ile Ile Phe	
275 280 285	
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Gly Ser Gln Trp Ser Ala Glu Glu Ala Gly Asp Gln Val Lys Val	
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Thr Leu Thr His Thr Tyr Tyr Leu Pro Lys Asp Asp Ala Lys Thr	
305 310 315	
agt caa ttc cta gaa cag att gac gct tac aag cga cct tct gaa	990
Ser Gln Phe Leu Glu Gln Ile Asp Ala Tyr Lys Atg Pro Ser Glu	
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Val Ala Lys Asp Gln Arg Gln Arg Arg Ser Arg Ser Lys Ser Ala	
335 340 345	
gat aag aag cct gag gag ttg tct gta act ctt gtg gag gca tac	1080
Asp Lys Lys Pro Glu Glu Lys Ser Val Thr Leu Val Glu Ala Tyr	
350 355 360	
aca gat gtg ttt gat gac aca cag gtt gag atg att gat gag gtt	1125
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Thr Asn	

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 <212> DNA  
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<220>

<223>

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Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu	
1 5 10 15	
tcg tgg aac tta gcg ttt ctg gtg ggg atc tta ttt aca ata gac	140
Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp	
20 25 30	
ata gga atg gcc aat cct agt cca cac caa ata tat aat gta act	185
Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr	
35 40 45	
tgg gta ata acc aat gta caa act aac acc caa gct aac gcc acc	230
Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr	
50 55 60	
tct atg tta gga acc tta acc gat gcc tac cct acc cta cat gtt	275
Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val	
65 70 75	
gac tta tgt gac cta gtg gga gac acc tgg gaa cct ata gtc cta	320
Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu	
80 85 90	
aac cca acc aat gta aaa cac ggg gca cgt tac tcc tcc tca aaa	365
Asn Pro Thr Asn'Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys	
95 100 105	
tat gga tgt aaa act aca gat aga aaa aaa cag caa cag aca tac	410
Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr	
110 115 120	
ccc ttt tac gtc tgc ccc gga cat gcc ccc tcg ttg ggg cca aag	455
Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys	
125 130 135	
gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg	500
Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp	
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Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser	
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Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser	
170 175 180	
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Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys	

185	190	195	
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cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser 215	220	225	725
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cca agg tct gtt gcc ccc acc acc atg ggt ccc aaa cgg att ggg Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly 275	280	285	905
acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala 290	295	300	950
tta aat gcc acc gac ccc aac aaa act aaa gac tgt tgg ctc tgc Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys 305	310	315	995
ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly 320	325	330	1040
acc tac agc aac caa aca aac ccc ccc cca tcc tgc cta tct act Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile 335	340	345	1085
ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met 350	355	360	1130
tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys 365	370	375	1175
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Leu	Trp	Pro	Arg	Val	Thr	Tyr	His	Gln	Pro	Glu	Tyr	Val	Tyr	Thr	
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His	Phe	Ala	Lys	Ala	Val	Arg	Phe	Arg	Arg	Glu	Pro	Ile	Ser	Leu	
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acg	gtt	gcc	ctt	atg	ttg	gga	gga	ctt	act	gta	ggg	ggc	ata	gcc	1445
Thr	Val	Ala	Leu	Met	Leu	Gly	Gly	Leu	Thr	Val	Gly	Gly	Ile	Ala	
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Ala	Gly	Val	Gly	Thr	Gly	Thr	Lys	Ala	Leu	Leu	Glu	Thr	Ala	Gln	
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Phe	Arg	Gln	Leu	Gln	Met	Ala	Met	His	Thr	Asp	Ile	Gln	Ala	Leu	
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gaa	gaa	tca	att	agt	gcc	tta	gaa	aag	tcc	ctg	acc	tcc	ctt	tct	1580
Glu	Glu	Ser	Ile	Ser	Ala	Leu	Glu	Lys	Ser	Leu	Thr	Ser	Leu	Ser	
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Glu	Val	Val	Leu	Gln	Asn	Arg	Arg	Glu	Leu	Asp	Ile	Leu	Phe	Leu	
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caa	gag	gga	ggg	ctc	tgt	gcc	gca	ttg	aaa	gaa	gaa	tgt	tgc	ttc	1670
Gln	Glu	Gly	Gly	Leu	Cys	Ala	Ala	Leu	Lys	Glu	Glu	Cys	Cys	Phe	
				530					535				540		
tat	gct	gat	cac	acc	gga	ctc	gtc	cga	gac	aat	atg	gcc	aaa	tta	1715
Tyr	Ala	Asp	His	Thr	Gly	Leu	Val	Arg	Asp	Asn	Met	Ala	Lys	Leu	
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Arg	Glu	Arg	Leu	Lys	Gln	Arg	Gln	Gln	Leu	Phe	Asp	Ser	Gln	Gln	
				560					565				570		
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Gly	Trp	Phe	Glu	Gly	Trp	Phe	Asn	Lys	Ser	Pro	Trp	Phe	Thr	Thr	
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cta	att	tcc	tcc	att	atg	ggc	ccc	tta	cta	atc	cta	ctc	cta	att	1850
Leu	Ile	Ser	Ser	Ile	Met	Gly	Pro	Leu	Leu	Ile	Leu	Leu	Ile	Ile	
				590					595				600		

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Leu Leu Phe Gly Pro Cys Ile Leu Asn Arg Leu Val Gln Phe Val  
605 610 615

aaa gac aga ata tct gtg gta cag gct tta att tta acc caa cag 1940  
Lys Asp Axa Ile Ser Val Val Gln Ala Leu Ile Leu Thr Gln Gln  
620 625 630

tac caa cag ata aag caa tac gat ccg gac cga cca tga 1979  
Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp Arg Pro  
635 640

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